

Exhibit A**Blast 2 Sequences results**

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.13 [Nov-27-2005]

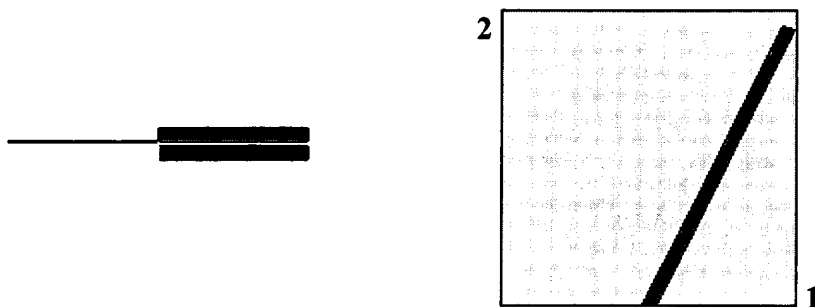
Matrix **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☒ View option **Standard**
Masking character option **X for protein, n for nucleotide** Masking color option **Black**
☐ Show CDS translation **Align**

Sequence 1: lcl|seq_1

Length = 28 (1 .. 28)

Sequence 2: lcl|seq_2

Length = 14 (1 .. 14)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

Score = 38.1 bits (87), Expect = 0.094
Identities = 14/14 (100%), Positives = 14/14 (100%), Gaps = 0/14 (0%)

Query 15 AGCKNFFWKFTSC 28
AGCKNFFWKFTSC
Sbjct 1 AGCKNFFWKFTSC 14

CPU time: 0.02 user secs. 0.01 sys. secs 0.03 total secs.

Lambda K H
0.320 0.125 0.434

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 16
Number of extensions: 5
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 28
Length of database: 1,129,354,045
Length adjustment: 3
Effective length of query: 25
Effective length of database: 1,129,354,042
Effective search space: 28233851050
Effective search space used: 28233851050
Neighboring words threshold: 9
X1: 16 (7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.9 bits)
S2: 70 (31.6 bits)